

SEQUENCE LISTING

<110> Seikagaku Corporation

<120> Catalyst for cleaving sugar chain

<130> Q90646

<140> US 10/551,550

<141> 2005-09-30

<150> PCT/JP2004/004695

<151> 2004-03-31

<150> JP 2003-097301

<151> 2003-03-31

<150> JP 2003-113965

<151> 2003-04-18

<160> 2

<170> PatentIn version 3.1

<210> 1

<211> 1308

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1308)

<400> 1

```

atg gca gcc cac ctg ctt ccc atc tgc gcc ctc ttc ctg acc tta ctc      48
Met Ala Ala His Leu Leu Pro Ile Cys Ala Leu Phe Leu Thr Leu Leu
1          5          10          15
gat atg gcc caa ggc ttt agg ggc ccc ttg cta ccc aac cgg ccc ttc      96
Asp Met Ala Gln Gly Phe Arg Gly Pro Leu Leu Pro Asn Arg Pro Phe
20          25          30
acc acc gtc tgg aat gca aac acc cag tgg tgc ctg gag agg cac ggt      144
Thr Thr Val Trp Asn Ala Asn Thr Gln Trp Cys Leu Glu Arg His Gly
35          40          45
gtg gac gtg gat gtc agt gtc ttc gat gtg gta gcc aac cca ggg cag      192
Val Asp Val Asp Val Ser Val Phe Asp Val Val Ala Asn Pro Gly Gln
50          55          60
acc ttc cgc ggc cct gac atg aca att ttc tat agc tcc cag ctg ggc      240
Thr Phe Arg Gly Pro Asp Met Thr Ile Phe Tyr Ser Ser Gln Leu Gly
65          70          75          80
acc tac ccc tac tac acg ccc act ggg gag cct gtg ttt ggt ggt ctg      288
Thr Tyr Pro Tyr Tyr Thr Pro Thr Gly Glu Pro Val Phe Gly Gly Leu
85          90          95
ccc cag aat gcc agc ctg att gcc cac ctg gcc cgc aca ttc cag gac      336
Pro Gln Asn Ala Ser Leu Ile Ala His Leu Ala Arg Thr Phe Gln Asp
100         105         110
atc ctg gct gcc ata cct gct cct gac ttc tca ggg ctg gca gtc atc      384
Ile Leu Ala Ala Ile Pro Ala Pro Asp Phe Ser Gly Leu Ala Val Ile

```

	115		120		125	
gac tgg gag gca tgg cgc cca cgc tgg gcc ttc aac tgg gac acc aag						432
Asp Trp Glu Ala Trp Arg Pro Arg Trp Ala Phe Asn Trp Asp Thr Lys						
	130		135		140	
gac att tac cgg cag cgc tca cgg gca ctg gta cag gca cag cac cct						480
Asp Ile Tyr Arg Gln Arg Ser Arg Ala Leu Val Gln Ala Gln His Pro						
	145		150		155	160
gat tgg cca gct cct cag gtg gag gca gta gcc cag gac cag ttc cag						528
Asp Trp Pro Ala Pro Gln Val Glu Ala Val Ala Gln Asp Gln Phe Gln						
		165		170		175
gga gct gca cgg gcc tgg atg gca ggc acc ctc cag ctg ggg cgg gca						576
Gly Ala Ala Arg Ala Trp Met Ala Gly Thr Leu Gln Leu Gly Arg Ala						
		180		185		190
ctg cgt cct cgc ggc ctc tgg ggc ttc tat ggc ttc cct gac tgc tac						624
Leu Arg Pro Arg Gly Leu Trp Gly Phe Tyr Gly Phe Pro Asp Cys Tyr						
	195		200		205	
aac tat gac ttt cta agc ccc aac tac acc ggc cag tgc cca tca ggc						672
Asn Tyr Asp Phe Leu Ser Pro Asn Tyr Thr Gly Gln Cys Pro Ser Gly						
	210		215		220	
atc cgt gcc caa aat gac cag cta ggg tgg ctg tgg ggc cag agc cgt						720
Ile Arg Ala Gln Asn Asp Gln Leu Gly Trp Leu Trp Gly Gln Ser Arg						
	225		230		235	240
gcc ctc tat ccc agc atc tac atg ccc gca gtg ctg gag ggc aca ggg						768
Ala Leu Tyr Pro Ser Ile Tyr Met Pro Ala Val Leu Glu Gly Thr Gly						
		245		250		255
aag tca cag atg tat gtg caa cac cgt gtg gcc gag gca ttc cgt gtg						816
Lys Ser Gln Met Tyr Val Gln His Arg Val Ala Glu Ala Phe Arg Val						
	260		265		270	
gct gtg gct gct ggt gac ccc aat ctg ccg gtg ctg ccc tat gtc cag						864
Ala Val Ala Ala Gly Asp Pro Asn Leu Pro Val Leu Pro Tyr Val Gln						
	275		280		285	
atc ttc tat gac acg aca aac cac ttt ctg ccc ctg gat gag ctg gag						912
Ile Phe Tyr Asp Thr Thr Asn His Phe Leu Pro Leu Asp Glu Leu Glu						
	290		295		300	
cac agc ctg ggg gag agt gcg gcc cag ggg gca gct gga gtg gtg ctc						960
His Ser Leu Gly Glu Ser Ala Ala Gln Gly Ala Ala Gly Val Val Leu						
	305		310		315	320
tgg gtg agc tgg gaa aat aca aga acc aag gaa tca tgt cag gcc atc						1008
Trp Val Ser Trp Glu Asn Thr Arg Thr Lys Glu Ser Cys Gln Ala Ile						
	325		330		335	
aag gag tat atg gac act aca ctg ggg ccc ttc atc ctg aac gtg acc						1056
Lys Glu Tyr Met Asp Thr Thr Leu Gly Pro Phe Ile Leu Asn Val Thr						
	340		345		350	
agt ggg gcc ctt ctc tgc agt caa gcc ctg tgc tcc ggc cat ggc cgc						1104
Ser Gly Ala Leu Leu Cys Ser Gln Ala Leu Cys Ser Gly His Gly Arg						
	355		360		365	
tgt gtc cgc cgc acc agc cac ccc aaa gcc ctc ctc ctc ctt aac cct						1152
Cys Val Arg Arg Thr Ser His Pro Lys Ala Leu Leu Leu Asn Pro						
	370		375		380	
gcc agt ttc tcc atc cag ctc acg cct ggt ggt ggg ccc ctg agc ctg						1200
Ala Ser Phe Ser Ile Gln Leu Thr Pro Gly Gly Gly Pro Leu Ser Leu						
	385		390		395	400
cgg ggt gcc ctc tca ctt gaa gat cag gca cag atg gct gtg gag ttc						1248
Arg Gly Ala Leu Ser Leu Glu Asp Gln Ala Gln Met Ala Val Glu Phe						
	405		410		415	
aaa tgt cga tgc tac cct ggc tgg cag gca ccg tgg tgt gag cgg aag						1296

Lys Cys Arg Cys Tyr Pro Gly Trp Gln Ala Pro Trp Cys Glu Arg Lys
 420 425 430
 agc atg tgg tga
 Ser Met Trp
 435

1308

<210> 2
 <211> 435
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Ala Ala His Leu Leu Pro Ile Cys Ala Leu Phe Leu Thr Leu Leu
 1 5 10 15
 Asp Met Ala Gln Gly Phe Arg Gly Pro Leu Leu Pro Asn Arg Pro Phe
 20 25 30
 Thr Thr Val Trp Asn Ala Asn Thr Gln Trp Cys Leu Glu Arg His Gly
 35 40 45
 Val Asp Val Asp Val Ser Val Phe Asp Val Val Ala Asn Pro Gly Gln
 50 55 60
 Thr Phe Arg Gly Pro Asp Met Thr Ile Phe Tyr Ser Ser Gln Leu Gly
 65 70 75 80
 Thr Tyr Pro Tyr Tyr Thr Pro Thr Gly Glu Pro Val Phe Gly Gly Leu
 85 90 95
 Pro Gln Asn Ala Ser Leu Ile Ala His Leu Ala Arg Thr Phe Gln Asp
 100 105 110
 Ile Leu Ala Ala Ile Pro Ala Pro Asp Phe Ser Gly Leu Ala Val Ile
 115 120 125
 Asp Trp Glu Ala Trp Arg Pro Arg Trp Ala Phe Asn Trp Asp Thr Lys
 130 135 140
 Asp Ile Tyr Arg Gln Arg Ser Arg Ala Leu Val Gln Ala Gln His Pro
 145 150 155 160
 Asp Trp Pro Ala Pro Gln Val Glu Ala Val Ala Gln Asp Gln Phe Gln
 165 170 175
 Gly Ala Ala Arg Ala Trp Met Ala Gly Thr Leu Gln Leu Gly Arg Ala
 180 185 190
 Leu Arg Pro Arg Gly Leu Trp Gly Phe Tyr Gly Phe Pro Asp Cys Tyr
 195 200 205
 Asn Tyr Asp Phe Leu Ser Pro Asn Tyr Thr Gly Gln Cys Pro Ser Gly
 210 215 220
 Ile Arg Ala Gln Asn Asp Gln Leu Gly Trp Leu Trp Gly Gln Ser Arg
 225 230 235 240
 Ala Leu Tyr Pro Ser Ile Tyr Met Pro Ala Val Leu Glu Gly Thr Gly
 245 250 255
 Lys Ser Gln Met Tyr Val Gln His Arg Val Ala Glu Ala Phe Arg Val
 260 265 270
 Ala Val Ala Ala Gly Asp Pro Asn Leu Pro Val Leu Pro Tyr Val Gln
 275 280 285
 Ile Phe Tyr Asp Thr Thr Asn His Phe Leu Pro Leu Asp Glu Leu Glu
 290 295 300
 His Ser Leu Gly Glu Ser Ala Ala Gln Gly Ala Ala Gly Val Val Leu
 305 310 315 320
 Trp Val Ser Trp Glu Asn Thr Arg Thr Lys Glu Ser Cys Gln Ala Ile
 325 330 335
 Lys Glu Tyr Met Asp Thr Thr Leu Gly Pro Phe Ile Leu Asn Val Thr

			340					345				350			
Ser	Gly	Ala	Leu	Leu	Cys	Ser	Gln	Ala	Leu	Cys	Ser	Gly	His	Gly	Arg
		355						360				365			
Cys	Val	Arg	Arg	Thr	Ser	His	Pro	Lys	Ala	Leu	Leu	Leu	Leu	Asn	Pro
		370					375					380			
Ala	Ser	Phe	Ser	Ile	Gln	Leu	Thr	Pro	Gly	Gly	Gly	Pro	Leu	Ser	Leu
385					390					395					400
Arg	Gly	Ala	Leu	Ser	Leu	Glu	Asp	Gln	Ala	Gln	Met	Ala	Val	Glu	Phe
				405					410					415	
Lys	Cys	Arg	Cys	Tyr	Pro	Gly	Trp	Gln	Ala	Pro	Trp	Cys	Glu	Arg	Lys
			420					425					430		
Ser	Met	Trp													
			435												